

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:05:08 ; Search time 193 Seconds  
(without alignments)  
89.436 Million cell updates/sec

Title: US-10-634-740-18  
Perfect score: 146  
Sequence: 1 ARTKQTARKSTGGKAPRKQLATYKARKSAP 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	38	2	024165 nicotiana t
2	146	100.0	39	2	092167 cricetus
3	146	100.0	48	2	Q7M327 patellinus
4	146	100.0	48	2	Q7M328 patella gra
5	146	100.0	48	2	Q7M1P0 encephalart
6	146	100.0	50	2	06Q4U0 valonia ex
7	146	100.0	50	2	06Q4U4 valonia pu
8	146	100.0	50	2	06Q4U6 valonia en
9	146	100.0	50	2	06Q4U8 valonia co
10	146	100.0	50	2	06Q4V0 ena montana
11	146	100.0	50	2	06Q4V2 acanthinula
12	146	100.0	50	2	06Q4V8 vertigo ant
13	146	100.0	50	2	06Q4W2 cochlicopa
14	146	100.0	50	2	06Q4W4 cochlicopa
15	146	100.0	50	2	06Q4W6 cochlicopa
16	146	100.0	50	2	06Q4W8 pupilla mus
17	146	100.0	50	2	06Q4X4 columella e
18	146	100.0	50	2	06Q4X6 truncatelli
19	146	100.0	50	2	06Q4X8 azeca gooda
20	146	100.0	50	2	06Q4Y0 cochliodina
21	146	100.0	50	2	06Q4Y2 punctum pyg
22	146	100.0	50	2	06Q4Y4 trichia vil
23	146	100.0	50	2	06Q4Y6 succinea pu
24	146	100.0	50	2	AAS55790 succinea
25	146	100.0	50	2	AAS55792 succinea
26	146	100.0	50	2	AAS55794 trichia v
27	146	100.0	50	2	AAS55796 punctum p
28	146	100.0	50	2	AAS55798 cochlidin
29	146	100.0	50	2	AAS55800 azeca goo
30	146	100.0	50	2	AAS55802 truncatel
31	146	100.0	50	2	AAS55804 columella

32	146	100.0	50	2	AAS55806 columella
33	146	100.0	50	2	AAS55808 columella
34	146	100.0	50	2	AAS55810 pupilla m
35	146	100.0	50	2	AAS55812 cochlicop
36	146	100.0	50	2	AAS55814 cochlicop
37	146	100.0	50	2	AAS55816 cochlicop
38	146	100.0	50	2	AAS55818 cochlicop
39	146	100.0	50	2	AAS55820 vertigo a
40	146	100.0	50	2	AAS55822 vertigo a
41	146	100.0	50	2	AAS55824 vertigo a
42	146	100.0	50	2	AAS55826 acanthinu
43	146	100.0	50	2	AAS55828 ena monta
44	146	100.0	50	2	AAS55830 valonia
45	146	100.0	50	2	AAS55832 valonia

## ALIGNMENTS

RESULT 1					
ID	024165	PRELIMINARY;	PRT;	38 AA.	
AC	024165;				
DT	01-JAN-1998 (TREMREL. 05, Created)				
DT	01-JAN-1998 (TREMREL. 05, Last sequence update)				
DT	01-MAR-2004 (TREMREL. 26, Last annotation update)				
DS	Histone H3 (Fragment).				
OS	Nicotiana tabacum (Common tobacco).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;				
OC	lamiales; Solanales; Solanaceae; Nicotiana.				
OX	NCBI_TaxID=4097;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bright Yellow 2;				
RX	(MEDLINE=98292547; PubMed=9628927;				
RA	Reichheld J.P.; Gigot C.; Chaubet-Gigot N.;				
RT	"Multilevel regulation of histone gene expression during the cell				
RT	cycle in plant cells.";				
RL	Nucleic Acids Res. 26:3255-3262(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Bright Yellow 2;				
RA	Chaubet N.;				
RL	Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; Y14195; CAA74582.1; -.				
DR	PIR; S56707; S56707.				
DR	GO; GO:000786; C:nucleosome; IEA.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003677; F:DNA binding; IEA.				
DR	GO; GO:007001; P:chromosome organization and biogenesis (gen. . .; IEA.				
DR	GO; GO:0006334; P:nucleosome assembly; IEA.				
DR	InterPro; IPR009072; Histone-H3.				
DR	InterPro; IPR00164; Histone_H3.				
DR	PRINTS; PR00622; HISTONEH3.				
DR	PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.				
FT	NOV_TER 38				
SQ	SEQUENCE 38 AA; 3939 MW; E1600FC8D9EDD8D3 CRC64;				
Query Match 100.0%; Score 146; DB 2; Length 38;					
Best local Similarity 100.0%; Pred. No. 1e-12;					
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 ARTKQTARKSTGGKAPRKQLATYKARKSAP 30				
DB	2 ARTKQTARKSTGGKAPRKQLATYKARKSAP 31				
RESULT 2					
ID	0921G7	PRELIMINARY;	PRT;	39 AA.	
AC	0921G7;				
DT	01-MAY-1999 (TREMREL. 10, Created)				

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DT 01-MAY-1999 (TReMBLrel. 10, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE H3.2 protein (fragment).
GN Name=H3.2;
OS Crictetus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Crictetinae;
OC Crictetulus.
OX NCBI_TaxID=10031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87315341; PubMed=3627229;
RA Artshemsky A., Wooden S., Sharma A., Resendez E.Jr., Lee A.S.;
RT "Cell-cycle regulatory sequences in a hamster histone promoter and
RL their interactions with cellular factors.";
DR EMBL; M28265; AAA42371.1; -.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .; IEA.
DR InterPro; IPR009072; Histone-fold.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 39
SQ SEQUENCE 39 AA; 4036 MW; DA31600FC8DEDD8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 146; DB 2; Length 39;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
    |||||
Db 2 ARTKOTARKSTGKAPRKQATKARKSAP 31

RESULT 3
QY 07M327 PRELIMINARY; PRT; 48 AA.
AC Q7M327;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Histone H3 (fragment).
OS Parechinus angulosus (Angulate sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Echinidae; Parechinus.
OX NCBI_TaxID=7658;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.";
RL FEBS Lett. 40:167-172(1974).
DR PIR; A61286; A61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .; IEA.
DR InterPro; IPR00164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 48
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;

Query Match
Best Local Similarity 100.0%; Score 146; DB 2; Length 48;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.0%; Score 146; DB 2; Length 48;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
    |||||
Db 1 ARTKOTARKSTGKAPRKQATKARKSAP 30

RESULT 4
QY 07M328 PRELIMINARY; PRT; 48 AA.
AC Q7M328;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Histone H3 (fragment).
OS Patella granatina (Sandpiper limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Eogastropoda; Docoglossa;
OC Patelina; Patelioidea; Patelidae; Patella.
OX NCBI_TaxID=6464;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.";
RL FEBS Lett. 40:167-172(1974).
DR PIR; B61286; B61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .; IEA.
DR InterPro; IPR00164; Histone_H3.
DR PRINTS; PR00622; HISTONEH3.
DR PROSITE; PS00322; HISTONE_H3_1; UNKNOWN_1.
FT NON TER 48
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;

Query Match
Best Local Similarity 100.0%; Score 146; DB 2; Length 48;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPRKQATKARKSAP 30
    |||||
Db 1 ARTKOTARKSTGKAPRKQATKARKSAP 30

RESULT 5
QY 07M1P0 PRELIMINARY; PRT; 48 AA.
AC Q7M1P0;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Histone H3 (fragment).
OS Eucephalartos caffer (Kaffir bread).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Cycadophyta; Cycadales; Zamiales; Eucephalartos.
OX NCBI_TaxID=36013;
RN [1]
RP SEQUENCE.
RX MEDLINE=74299572; PubMed=4851114;
RA Brandt W.F., Strickland W.N., Morgan M., Von Holt C.;
RT "Comparison of the N-terminal amino acid sequences of histone F3 from
RT a mammal, a bird, a shark, an echinoderm, a mollusc and a plant.";
RL FEBS Lett. 40:167-172(1974).
DR PIR; C61286; C61286.
DR GO; GO:0000786; C:nucleosome; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .; IEA.
DR InterPro; IPR00164; Histone_H3.
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DR PRINTS: PR00622; HISTONEH3.  
DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
FT NON TER 1 48  
FT NON TER 48  
SQ SEQUENCE 48 AA; 5056 MW; 8C4505BF726ESD38 CRC64;  
Query Match 100.0%; Score 146; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

RESULT 6  
Q6Q4U0 PRELIMINARY; PRT; 50 AA.  
ID Q6Q4U0  
AC Q6Q4U0;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Histone H3 (Fragment).  
OS Vallonia excentrica.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Orthurethra; Pupillioidea; Valloniidae; Vallonia.  
CX NCB1\_TaxID=145447;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY559169; AAS55838.1; -  
DR InterPro; IPR009072; Histone-Fold.  
DR InterPro; IPR000164; Histone\_H3.  
DR PRINTS; PR00622; HISTONEH3.  
DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
FT NON TER 50  
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 7  
Q6Q4U4 PRELIMINARY; PRT; 50 AA.  
ID Q6Q4U4  
AC Q6Q4U4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Histone H3 (Fragment).  
OS Vallonia pulchella.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Orthurethra; Pupillioidea; Valloniidae; Vallonia.  
CX NCB1\_TaxID=229284;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY559167; AAS55834.1; -  
DR EMBL; AY559168; AAS55836.1; -  
DR InterPro; IPR009072; Histone-Fold.  
DR InterPro; IPR000164; Histone\_H3.  
DR PRINTS; PR00622; HISTONEH3.  
DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
FT NON TER 50  
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 8  
Q6Q4U6 PRELIMINARY; PRT; 50 AA.  
ID Q6Q4U6  
AC Q6Q4U6;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Histone H3 (Fragment).  
OS Vallonia enliensis.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Orthurethra; Pupillioidea; Valloniidae; Vallonia.  
CX NCB1\_TaxID=229285;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY559166; AAS55832.1; -  
DR InterPro; IPR009072; Histone-Fold.  
DR InterPro; IPR000164; Histone\_H3.  
DR PRINTS; PR00622; HISTONEH3.  
DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
FT NON TER 50  
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 9  
Q6Q4U8 PRELIMINARY; PRT; 50 AA.  
ID Q6Q4U8  
AC Q6Q4U8;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Histone H3 (Fragment).  
OS Vallonia costata.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Orthurethra; Pupillioidea; Valloniidae; Vallonia.  
CX NCB1\_TaxID=145157;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY559165; AAS55830.1; -  
DR InterPro; IPR009072; Histone-Fold.  
DR InterPro; IPR000164; Histone\_H3.  
DR PRINTS; PR00622; HISTONEH3.  
DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
FT NON TER 50  
SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426ESD CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1,3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30

Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 10

06Q4V0

AC 06Q4V0; PRELIMINARY; PRT; 50 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE Histone H3 (Fragment).

OS Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC NCB1\_TaxID=265227; Enidae; Ena.

RP SEQUENCE FROM N.A.

RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY559164; AAS55828.1; -

DR InterPro; IPR009072; Histone-fold.

DR PRINTS; PR00622; HISTONEH3.

DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.

FT NON TER 50

SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 11

06Q4V2

AC 06Q4V2; PRELIMINARY; PRT; 50 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE Histone H3 (Fragment).

OS Acanthinula aculeata.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Orthurethra; Pupilloidea; Valloniidae; Acanthinula.

OC NCB1\_TaxID=229287; [1]

RP SEQUENCE FROM N.A.

RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY559163; AAS55826.1; -

DR InterPro; IPR009072; Histone-fold.

DR PRINTS; PR00622; HISTONEH3.

DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.

FT NON TER 50

SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 12

06Q4V8

ID 06Q4V8; PRELIMINARY; PRT; 50 AA.

AC 06Q4V8;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE Histone H3 (Fragment).

OS Vertigo antvertigo.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Orthurethra; Pupilloidea; Vertiginidae; Vertigo.

OC NCB1\_TaxID=145162; [1]

RP SEQUENCE FROM N.A.

RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY559160; AAS55820.1; -

DR EMBL; AY559161; AAS55822.1; -

DR EMBL; AY559162; AAS55824.1; -

DR InterPro; IPR009072; Histone-fold.

DR PRINTS; PR00622; HISTONE\_H3.

DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.

FT NON TER 50

SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 13

06Q4W2

ID 06Q4W2; PRELIMINARY; PRT; 50 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE Histone H3 (Fragment).

OS Cochlicopa lubrica.

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Orthurethra; Cochlicopoidae; Cochlicopidae; Cochlicopa.

OC NCB1\_TaxID=82567; [1]

RP SEQUENCE FROM N.A.

RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY559158; AAS55816.1; -

DR EMBL; AY559159; AAS55818.1; -

DR InterPro; IPR009072; Histone-fold.

DR PRINTS; PR00622; HISTONE\_H3.

DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.

FT NON TER 50

SQ SEQUENCE 50 AA; 5343 MW; 541518B31D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKOTARKSTGGKAPRKQATKAARKSAP 30  
Db 2 ARTKOTARKSTGGKAPRKQATKAARKSAP 31

RESULT 14

06Q4W4

ID 06Q4W4; PRELIMINARY; PRT; 50 AA.

AC 06Q4W4;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE Histone H3 (Fragment).

OS Cochlicopa lubricella.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Orchuethra; Cochlicopidae; Cochlicopidae; Cochlicopa.  
 CX NCBI\_TaxID=82566;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY559157; AAS55814.1; -.  
 DR InterPro; IPR009072; Histone-Fold.  
 DR InterPro; IPR00164; Histone\_H3.  
 DR PRINTS; PR00622; HISTONEH3.  
 DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
 FT NON TER 50  
 SQ SEQUENCE 50 AA; 5343 MW; 54151831D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
 |||  
 Db 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

## RESULT 15

ID Q6Q4W6 PRELIMINARY; PRT; 50 AA.  
 AC Q6Q4W6;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Histone H3 (fragment).  
 OS Cochlicopa nitens.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Orchuethra; Cochlicopidae; Cochlicopidae; Cochlicopa.  
 CX NCBI\_TaxID=82566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Armbruster G., Boehme M., Bernhard D., Schlegel M.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY559156; AAS55812.1; -.  
 DR InterPro; IPR009072; Histone-Fold.  
 DR InterPro; IPR00164; Histone\_H3.  
 DR PRINTS; PR00622; HISTONEH3.  
 DR PROSITE; PS00322; HISTONE\_H3\_1; UNKNOWN\_1.  
 FT NON TER 50  
 SQ SEQUENCE 50 AA; 5343 MW; 54151831D426E5D CRC64;

Query Match 100.0%; Score 146; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
 |||  
 Db 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

Search completed: December 23, 2004, 11:22:04  
 Job time : 194 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 11:16:09 ; Search time 38 Seconds

(without alignments)  
52.356 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 446  
Sequence: 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	72	4	US-09-621-976-7473
2	146	100.0	108	4	US-09-513-999C-5370
3	146	100.0	136	4	US-09-621-976-7472
4	146	100.0	136	4	US-09-976-594-1029
5	142	97.3	152	4	US-09-248-786A-18649
6	99	67.8	20	3	US-09-451-034-13
7	99	67.8	20	4	US-09-876-221-7
8	99	67.8	20	4	US-09-589-892B-19
9	64	43.8	13	3	US-09-451-034-8
10	58.5	40.1	214	3	US-09-041-889-27
11	58.5	40.1	214	4	US-09-417-264-27
12	58	39.7	12	3	US-09-451-034-7
13	56	38.4	93	4	US-09-270-767-39947
14	56	38.4	93	4	US-09-270-767-55164
15	54	37.0	375	1	US-08-363-255-7
16	54	37.0	528	1	US-08-363-255-14
17	54	37.0	530	1	US-08-363-255-2
18	54	37.0	530	1	US-08-363-255-3
19	54	37.0	530	1	US-08-363-255-8
20	54	37.0	530	1	US-08-363-255-9
21	54	37.0	530	1	US-08-363-255-10
22	52.5	36.0	442	1	US-08-363-255-4
23	52.5	36.0	442	1	US-08-363-255-11
24	52	35.6	156	4	US-09-252-991A-23987
25	52	35.6	223	3	US-09-095-855-201
26	52	35.6	223	4	US-09-205-426-201
27	51.5	35.3	302	4	US-09-252-991A-19529

28	51	34.9	96	4	US-09-252-991A-26685	Sequence 26685, A
29	51	34.9	236	4	US-09-252-991A-18461	Sequence 18461, A
30	51	34.9	310	1	US-08-363-255-6	Sequence 6, Appli
31	51	34.9	445	1	US-08-363-255-5	Sequence 5, Appli
32	51	34.9	445	1	US-08-363-255-12	Sequence 12, Appli
33	50.5	34.6	783	4	US-09-252-991A-18035	Sequence 18035, A
34	50	34.2	144	4	US-09-252-991A-17329	Sequence 17329, A
35	50	34.2	191	4	US-10-101-464A-753	Sequence 753, App
36	50	34.2	614	4	US-09-252-991A-28630	Sequence 28630, A
37	50	34.2	697	4	US-09-252-991A-24009	Sequence 24009, A
38	49.5	33.9	100	4	US-09-621-976-6834	Sequence 6834, Ap
39	49.5	33.9	409	4	US-09-252-991A-20892	Sequence 20892, A
40	49	33.6	13	3	US-09-451-034-3	Sequence 3, Appli
41	49	33.6	269	4	US-09-408-020-6	Sequence 6, Appli
42	49	33.6	507	4	US-09-252-991A-31473	Sequence 31473, A
43	49	33.6	580	4	US-08-311-731A-289	Sequence 289, App
44	49	33.6	1788	2	US-08-962-284-2	Sequence 2, Appli
45	48.5	33.2	176	4	US-09-252-991A-17546	Sequence 17546, A

#### ALIGNMENTS

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RESULT 1
US-09-621-976-7473
Sequence 7473, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OR INVENTION: Bsts and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7473
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 72
OTHER INFORMATION: Xaa = Gly,Arg,Tyr
US-09-621-976-7473

Query Match      100.0%; Score 146; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30
Db      2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

RESULT 2
US-09-513-999C-5370
Sequence 5370, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, RRG
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
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/ SEQ ID NO 5370
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 89
/ OTHER INFORMATION: Xaa=Ala or Pro
/ NAME/KEY: UNSURE
/ LOCATION: 99
/ OTHER INFORMATION: Xaa=Ala or Leu or Ser or Val
US-09-513-999C-5370
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Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 108;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATYKARKSAP 31
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RESULT 3
US-09-621-976-7472
/ Sequence 7472, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Ubert, S.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET 054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 7472
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 89
/ OTHER INFORMATION: Xaa = Ala,Pro
/ NAME/KEY: UNSURE
/ LOCATION: 99
/ OTHER INFORMATION: Xaa = Asn,Tyr
US-09-621-976-7472
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```
Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 136;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATYKARKSAP 31
```

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RESULT 4
US-09-976-594-1029
/ Sequence 1029, Application US/0976594
/ Patent No. 6673549
/ GENERAL INFORMATION:
/ APPLICANT: Furness, Michael
/ APPLICANT: Buchbinder Jenny
/ TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS
/ FILE REFERENCE: PA-0041 US
/ CURRENT APPLICATION NUMBER: US/09/976,594
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240,409
/ PRIOR FILING DATE: 2000-10-12
/ NUMBER OF SEQ ID NOS: 1143
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/ SOFTWARE: PERL Program
/ SEQ ID NO 1029
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incycle ID No. 6673549 4832672CD1
US-09-976-594-1029
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Query Match
Best Local Similarity 100.0%; Score 146; DB 4; Length 136;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATYKARKSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATYKARKSAP 31
```

```
RESULT 5
US-09-248-796A-18649
/ Sequence 18649, Application US/09248796A
/ Patent No. 6747137
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstock et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ CURRENT FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 18649
/ LENGTH: 152
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-18649
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Query Match
Best Local Similarity 97.3%; Score 142; DB 4; Length 152;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATYKARKSAP 30
Db 18 ARTKOTARKSTGGKAPRKQLATYKARKSAP 47
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```
RESULT 6
US-09-451-034-13
/ Sequence 13, Application US/09451034
/ Patent No. 6369030
/ GENERAL INFORMATION:
/ APPLICANT: Cole, Phillip et al
/ TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES
/ FILE REFERENCE: 600-1-265
/ CURRENT APPLICATION NUMBER: US/09/451,034
/ CURRENT FILING DATE: 1999-11-29
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
/ OTHER INFORMATION: MOLECULE THAT ACT AS ENZYME INHIBITOR
/ OTHER INFORMATION: The A in position 1 is a modified residue and is
/ OTHER INFORMATION: acetylated. The K in position 4 is a modified
/ OTHER INFORMATION: residue and is conjugated via its epsilon NH2
```



OTHER INFORMATION: group to coenzyme A.  
US-09-451-034-13

Query Match 67.8%; Score 99; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPPRKQL 20  
DB 1 ARTKQTARKSTGGKAPPRKQL 20

RESULT 7  
US-09-876-221-7

Sequence 7, Application US/09876221  
Patent No. 6555329  
GENERAL INFORMATION:  
APPLICANT: Jenuwein, Thomas  
APPLICANT: Rea, Stephen  
APPLICANT: Eisenhaber, Frank  
APPLICANT: O'Carroll, Donal  
TITLE OF INVENTION: Method for identifying compounds altering higher-order chromatin  
FILE REFERENCE: 0652.2240001  
CURRENT APPLICATION NUMBER: US/09/876,221  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: EP 00 112 345.4  
PRIOR FILING DATE: 2000-06-09  
PRIOR APPLICATION NUMBER: EP 00 112 479.1  
PRIOR FILING DATE: 2000-06-09  
PRIOR APPLICATION NUMBER: US 60/224,220  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-876-221-7

Query Match 67.8%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPPRKQL 20  
DB 1 ARTKQTARKSTGGKAPPRKQL 20

RESULT 8  
US-09-589-892B-19  
Sequence 19, Application US/09589892B  
Patent No. 6689583  
GENERAL INFORMATION:  
APPLICANT: Jenuwein, Thomas  
APPLICANT: Laible, Gocz  
APPLICANT: O'Carroll, Donal  
APPLICANT: Eisenhaber, Frank  
APPLICANT: Rea, Stephen  
TITLE OF INVENTION: Chromatin-Regulator Genes  
FILE REFERENCE: 0652.1670001  
CURRENT APPLICATION NUMBER: US/09/589,892B  
CURRENT FILING DATE: 2000-06-09  
PRIOR APPLICATION NUMBER: US 08/945,988  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: PCT/EP96/01818  
PRIOR FILING DATE: 1996-05-02  
PRIOR APPLICATION NUMBER: DE 195 16 776.7  
PRIOR FILING DATE: 1995-05-10  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 19  
LENGTH: 20

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-589-892B-19

Query Match 67.8%; Score 99; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPPRKQL 20  
DB 1 ARTKQTARKSTGGKAPPRKQL 20

RESULT 9  
US-09-451-034-8

Sequence 8, Application US/09451034  
Patent No. 6369030  
GENERAL INFORMATION:  
APPLICANT: Cole, Phillip et al  
TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES  
FILE REFERENCE: 600-1-265  
CURRENT APPLICATION NUMBER: US/09/451,034  
CURRENT FILING DATE: 1999-11-29  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PART OF  
OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
OTHER INFORMATION: The first ala is a modified residue; it is  
OTHER INFORMATION: acetylated.  
US-09-451-034-8

Query Match 43.8%; Score 64; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0044;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGG 13  
DB 1 ARTKQTARKSTGG 13

RESULT 10  
US-09-041-889-27  
Sequence 27, Application US/09041889  
Patent No. 6033864  
GENERAL INFORMATION:  
APPLICANT: Braun, Jonathan  
APPLICANT: Cohavy, Offer  
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,889  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/837,058  
FILING DATE: 11-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PM 3006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-041-889-27

Query Match 40.1%; Score 58.5; DB 3; Length 214;  
Best Local Similarity 55.2%; Pred. No. 0.58;  
Matches 16; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 29  
DB 130 AATKAPARKA-ATKAPAKKAAATKAPAKKA 157

RESULT 11  
US-09-417-264-27  
Sequence 27, Application US/09417264  
Patent No. 6537768  
GENERAL INFORMATION:  
APPLICANT: Braun, Jonathan  
APPLICANT: Conavy, Offer  
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of  
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using  
TITLE OF INVENTION: Microbial UC PANCA antigens  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/417,264  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/041,889  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-PM 3006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 214 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-417-264-27

Query Match 40.1%; Score 58.5; DB 4; Length 214;

Best Local Similarity 55.2%; Pred. No. 0.58;  
Matches 16; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 29  
DB 130 AATKAPARKA-ATKAPAKKAAATKAPAKKA 157

RESULT 12  
US-09-451-034-7  
Sequence 7, Application US/09451034  
Patent No. 6369030  
GENERAL INFORMATION:  
APPLICANT: Cole, Philip et al  
TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: 600-1-265  
CURRENT APPLICATION NUMBER: US/09/451,034  
CURRENT FILING DATE: 1999-11-29  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 7  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PART OF  
OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
OTHER INFORMATION: The first ala is a modified residue; it is  
US-09-451-034-7

Query Match 39.7%; Score 58; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTG 12  
DB 1 ARTKOTARKSTG 12

RESULT 13  
US-09-270-767-39947  
Sequence 39947, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 39947  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-270-767-39947

Query Match 38.4%; Score 56; DB 4; Length 93;  
Best Local Similarity 46.2%; Pred. No. 0.55;  
Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGKAPKQKATKARKSA 26  
DB 6 AKTHQAKKVLSPQDPKRLTTWVAR 31

RESULT 14  
US-09-270-767-55164  
Sequence 55164, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-084  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentn Ver. 2.0  
 ; SEQ ID NO 55164  
 ; LENGTH: 93  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-270-767-55164

Query March 38.4%; Score 56; DB 4; Length 93;  
 Best Local Similarity 46.2%; Pred. No. 0.55;  
 Matches 12; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 ARTKQAKSTGKAPRKQATKAAR 26  
 DB 6 AKTHQAKKVLSPQDPKRLTTWVAR 31

RESULT 15  
 US-08-363-255-7  
 ; Sequence 7, Application US/08363255  
 ; Patent No. 5783386  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JACOBS, Jr., WILLIAM R.  
 ; APPLICANT: BLOOM, BARRY R.  
 ; APPLICANT: COLLINS, DESMOND M.  
 ; APPLICANT: de LISLE, GEOFFREY W.  
 ; APPLICANT: PASCOPELLA, LISA  
 ; APPLICANT: KAKAKAMI, RIKU P.  
 ; TITLE OF INVENTION: MYCOBACTERIA VIRULENCE FACTORS AND A  
 ; NUMBER OF INVENTION: NOVEL METHOD FOR THEIR IDENTIFICATION  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESS: MORRISON & ROEBSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/363,255  
 ; FILING DATE: 23-DEC-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MONROY, GLADYS H.  
 ; REGISTRATION NUMBER: 32,430  
 ; REFERENCE/DOCKET NUMBER: 25237-20002.22  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 375 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-363-255-7

Query March 37.0%; Score 54; DB 1; Length 375;  
 Best Local Similarity 44.4%; Pred. No. 4.8;  
 Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;  
 QY 4 KQAKSTGKAPRKQATKAAR 30

DB 36 KRTAKASGSPPAKRAKPAKRSVKP 62

Search completed: December 23, 2004, 11:35:52  
 Job time : 42 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:04:22 / Search time 159 Seconds  
(without alignments)  
67.685 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 146  
Sequence: 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_23Sep04:\*

1: \_geneseqp1980s:\*\n2: \_geneseqp1990s:\*\n3: \_geneseqp2000s:\*\n4: \_geneseqp2001s:\*\n5: \_geneseqp2002s:\*\n6: \_geneseqp2003as:\*\n7: \_geneseqp2003bs:\*\n8: \_geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	30	6 ADA13508	Ada13508 Human H3
2	146	100.0	30	8 ADO21849	Ado21849 Human his
3	146	100.0	40	5 ABB07291	Abb07291 Human his
4	146	100.0	40	8 ADO21832	Ado21832 Human his
5	146	100.0	55	5 AAU70897	Aau70897 Histone 2
6	146	100.0	65	3 AAG07049	Aag07049 Arabidops
7	146	100.0	70	2 AAR46075	Aar46075 Histone H
8	146	100.0	81	3 AAG35461	Aag35461 Arabidops
9	146	100.0	90	3 AAG22671	Aag22671 Zea may
10	146	100.0	93	5 ABB42906	Abb42906 Human ova
11	146	100.0	95	3 AAG13239	Aag13239 Arabidops
12	146	100.0	108	3 AAG01289	Aag01289 Human sec
13	146	100.0	108	3 AAG54610	Aag54610 Zea may
14	146	100.0	109	3 AAG41100	Aag41100 Zea may
15	146	100.0	110	3 AAG27142	Aag27142 Zea may
16	146	100.0	113	3 AAG12241	Aag12241 Zea may
17	146	100.0	114	3 AAG44971	Aag44971 Zea may
18	146	100.0	117	3 AAG12552	Aag12552 Zea may
19	146	100.0	121	3 AAG12629	Aag12629 Zea may
20	146	100.0	121	3 AAG44980	Aag44980 Zea may
21	146	100.0	126	3 AAG12354	Aag12354 Zea may
22	146	100.0	130	3 AAG26892	Aag26892 Zea may
23	146	100.0	131	3 AAG27143	Aag27143 Zea may
24	146	100.0	134	2 AAU07284	Aau07284 Histone H
25	146	100.0	134	2 AAU05482	Aau05482 Consensus

26	146	100.0	135	2 AAU07285	AAU07285 Human his
27	146	100.0	135	2 AAU05483	AAU05483 Human his
28	146	100.0	135	7 ADE59324	Ade59324 Rat Prote
29	146	100.0	136	3 AAG43664	Aag43664 Arabidops
30	146	100.0	136	3 AAG47930	Aag47930 Arabidops
31	146	100.0	136	3 AAG07917	Aag07917 Arabidops
32	146	100.0	136	3 AAG41099	Aag41099 Zea may
33	146	100.0	136	3 AAG43813	Aag43813 Arabidops
34	146	100.0	136	3 AAG53143	Aag53143 Arabidops
35	146	100.0	136	3 AAG10324	Aag10324 Arabidops
36	146	100.0	136	3 AAG12084	Aag12084 Arabidops
37	146	100.0	136	3 AAG08768	Aag08768 Arabidops
38	146	100.0	136	3 AAG44415	Aag44415 Arabidops
39	146	100.0	136	3 AAG26219	Aag26219 Arabidops
40	146	100.0	136	3 AAG53145	Aag53145 Arabidops
41	146	100.0	136	3 AAG04323	Aag04323 Arabidops
42	146	100.0	136	3 AAG53099	Aag53099 Arabidops
43	146	100.0	136	4 AAM17089	Aam17089 Peptide #
44	146	100.0	136	4 ABB61842	Abb61842 Drosophi1
45	146	100.0	136	4 ABB64138	Abb64138 Drosophi1

## ALIGNMENTS

RESULT 1	
ADA13508	ADA13508 standard; peptide; 30 AA.
XX	ADA13508;
AC	ADA13508;
XX	20-NOV-2003 (first entry)
DT	
XX	Human H3 histone amino acid sequence.
DE	
XX	detection; active gene; inactive gene; antibody; modified histone;
KW	tumour suppressor; oncogene; human; histone; epilo.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key
FT	Modified-site 2 Location/Qualifiers
FT	Modified-site 4 /label= methylation
FT	Modified-site 9 /label= methylation
FT	Modified-site 10 /label= acetylation or methylation
FT	Modified-site 10 /label= phosphorylation
FT	Modified-site 14 /label= acetylation
FT	Modified-site 17 /label= acetylation
FT	Modified-site 18 /label= methylation
FT	Modified-site 23 /label= acetylation
FT	Modified-site 26 /label= acetylation
FT	Modified-site 27 /label= methylation
FT	Modified-site 28 /label= methylation
FT	Modified-site 28 /label= phosphorylation
XX	
PD	WO2003070894-A2.
XX	28-AUG-2003.
XX	
XX	19-FEB-2003; 2003WO-US004661.
XX	
XX	20-FEB-2002; 2002US-0358325P.
PR	19-MAR-2002; 2002US-0365459P.

XX (UVI-) UNIV VIRGINIA PATENT FOUND.  
 PA (CHRO-) CHROMA THERAPEUTICS LTD.  
 PI

XX Allie CD, Bruns DE, Drummond AH;  
 DR WPI, 2003-697607/66.

XX Detecting active or inactive gene sequences associated with modified  
 PT histones is useful to diagnose disease states, for example inactivation  
 of a tumor suppressor gene or activation of an oncogene.  
 PS

XX Disclosure, Fig 1, 34pp; English.

CC The present invention describes a method for detecting active or inactive  
 CC gene sequences in an individual. The method comprises: (a) contacting a  
 CC body fluid sample with an antibody that binds to a modified histone  
 CC associated with active or inactive gene sequences; (b) isolating  
 CC nucleosomes bound to the antibody; (c) purifying the DNA associated with  
 CC the nucleosomes; and (d) identifying a gene encoded by the purified DNA.  
 CC Also described: (1) detecting active gene sequences in an individual,  
 CC comprising: (i) contacting a body fluid sample with an antibody that  
 CC binds to a modified histone associated with active gene sequences; (ii)  
 CC isolating nucleosomes bound to the antibody; (iii) purifying the DNA  
 CC associated with the nucleosomes; and (iv) identifying a gene encoded by  
 CC the purified DNA; (2) detecting inactive gene sequences in an individual,  
 CC comprising: (i) contacting a body fluid sample with an antibody that  
 CC binds to a modified histone associated with inactive gene sequences; (ii)  
 CC isolating nucleosomes bound to the antibody; (iii) purifying the DNA  
 CC associated with the nucleosomes; and (iv) identifying a gene encoded by  
 CC the purified DNA; (3) isolating nucleosomes released from apoptotic cells  
 CC of an individual; (4) detecting chromatin alterations associated with a  
 CC disease state; and (5) detecting a disease state. The methods are useful  
 CC in diagnosing a disease state such as inactivation of a tumor suppressor  
 CC gene or the activation of an oncogene. The present sequence represents a  
 CC human H3 histone amino acid sequence, which is given in the  
 CC exemplification of the present invention.  
 XX

SO Sequence 30 AA;

Query Match 100.0%; Score 146; DB 6; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-13;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATTKAARKSAP 30  
 DB 1 ARTKOTARKSTGGKAPRKQLATTKAARKSAP 30

RESULT 2  
 ADO21849  
 ID ADO21849 standard; peptide: 30 AA.  
 XX  
 AC ADO21849;  
 XX  
 DT 12-AUG-2004 (first entry)

XX Human histone H3 N-terminal peptide (SEQ ID 18).  
 DE  
 XX  
 KW fusion protein reporter; histone modification; cytostatic;  
 KW neuroprotective; muscular; virucide; cancer; neurological;  
 KW muscular disorders; developmental; cell development; toxin;  
 KW toxic chemical; virus; human; histone H3; N-terminal.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 2 /note= "Post-translational modification methylation site"

FT Modified-site 4 /note= "Post-translational modification methylation site"

FT Modified-site 9 /note= "Post-translational modification methylation site"

FT Modified-site /note= "Post-translational modification methylation site"

PT methylation/acetylation site"  
 FT 10 /note= "Post-translational modification phosphorylation  
 FT site"  
 FT Modified-site 14 /note= "Post-translational modification acetylation site"  
 FT 17 /note= "Post-translational modification methylation site"  
 FT 18 /note= "Post-translational modification methylation site"  
 FT 23 /note= "Post-translational modification acetylation site"  
 FT 26, 27 /note= "Post-translational modification methylation site"  
 FT 28 /note= "Post-translational modification methylation site"  
 FT Modified-site /note= "Post-translational modification phosphorylation  
 FT site"

W02004044168-A2.

27-MAY-2004.

12-NOV-2003; 2003WO-US036059.

12-NOV-2002; 2002US-042578P.

05-AUG-2003; 2003US-00634740.

(MASI ) MASSACHUSETTS INST TECHNOLOGY.

Ting AY;

WPI, 2004-420310/39.

PT New fusion protein reporter having a core with a histone-modification-  
 PT specific binding domain conjugated to a histone polypeptide, useful for  
 PT diagnosing or treating cancer, viral infections, neurological and  
 PT muscular disorders.  
 XX

PS Claim 15; SEQ ID NO 18; 96pp; English.

CC The invention relates to a novel fusion protein reporter comprising a  
 CC core having a histone-modification-specific binding domain conjugated to  
 CC a histone polypeptide, wherein the core is flanked by donor and acceptor  
 CC fluorescent moieties. The molecules of the invention demonstrate  
 CC cytostatic, neuroprotective, muscular and virucide activities and may be  
 CC useful for the diagnosis and/or treatment of histone modification-  
 CC associated disorders, such as cancer, neurological disorders, muscular  
 CC disorders, developmental disorders, cell development disorders and  
 CC current sequence is that of the human histone H3 N-terminal peptide (SEQ  
 CC ID 18) of the invention.  
 XX

SO Sequence 30 AA;

Query Match 100.0%; Score 146; DB 8; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-13;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATTKAARKSAP 30  
 DB 1 ARTKOTARKSTGGKAPRKQLATTKAARKSAP 30

RESULT 3

AB07291  
 ID ABB07291 standard; peptide: 40 AA.

AC ABB07291;

DT 02-APR-2002 (first entry)

XX Human histone H3 protein amino terminal fragment.

KM	CENP-A-centromere-associated histone H3; variant; phosphorylation; H3;
KW	mitosis; meiosis; kinase inhibitor; cytostatic; human; cancer; marker.
XX	
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Modified-site 10 /note= "phosphorylated"
FT	Modified-site 28 /note= "phosphorylated"
PN	WO200192339-A1.
PD	06-DEC-2001.
PF	31-MAY-2001; 2001WO-US017633.
PR	31-MAY-2000; 2000US-0208261P.
PA	(UYVI-) UNIV VIRGINIA PATENT FOUND.
PA	(SCRI ) SCRIPPS RES INST.
PI	Allis CD, Sullivan KF;
DR	WPt; 2002-114331/15.
PT	Novel antibody directed against histone H3-like protein (CENP-A) that is
PT	phosphorylated at a specific position in the amino terminal part during
MX	mitosis in vivo, useful as marker of mitosis and in diagnostic imaging.
BS	Disclosure; Fig 1a; 50pp; English.
XX	
CC	The invention relates to an antibody, which is directed against amino
CC	terminal portion of CENP-A (a unique centromere-associated histone H3
CC	variant) that is phosphorylated (Phos CENP-A) or is unphosphorylated (Un
CC	CENP-A). Since CENP-A is selectively phosphorylated in vivo at the amino
CC	acid Ser at position 7 in the amino terminus during mitosis, anti-Phos
CC	CENP-A antibody is useful as a marker of cell mitosis and meiosis. The
CC	antibody which specifically binds to Phos CENP-A and coupled to a
CC	bioactive substance such as a drug, toxin, immunomodulator, a peptide
CC	effector or an isotope, is useful for treating cancer in humans. The
CC	antibody is also useful in screening for potential inhibitors of a
CC	kinase. The antibody provides a mitosis and/or proliferation marker that
CC	has research and diagnostic potential. Since the amount of detectable
CC	Phos CENP-A present in a cell varies throughout the cell cycle, the anti-
CC	Phos CENP-A antibody can also be used to determine the mitotic stage of a
CC	cell. The anti-Phos CENP-A antibody can be used for identifying tissues
CC	that contain a high incidence of mitotic cells and assist in detecting
CC	oncogenesis and cancer, and thus is useful for locating and diagnosing
CC	cancer in vivo. It can also be used for isolating mitotically dividing
CC	cells from complex mixtures. The present sequence represents the amino-
CC	terminal sequence of the human histone H3 protein
XX	
SQ	Sequence 40 AA;
Query Match	100.0%; Score 146; DB 5; Length 40;
Best Local Similarity	100.0%; Pred. No. 3,8e-13;
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ARTKOTARKSTGSKAPRQLATKARKSP 30       
DB	1 ARTKOTARKSTGSKAPRQLATKARKSP 30
RESULT 4	
ADO21832	
ID	ADO21832 standard; peptide; 40 AA.
XX	
AC	ADO21832;
XX	
DT	12-AUG--2004 (first entry)
DE	Human histone H3 N-terminal peptide (SEQ ID 1).

XX		fusion protein reporter; histone modification; cytosstatic;
KM		neuroprotective; muscular; virucide; cancer; neurological;
KM		muscular disorders; developmental; cell development; toxin;
KM		toxic chemical; virus; human; histone H3; N-terminal.
OS		Homo sapiens.
XX		
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	8 /note= "Post-translational modification acetylation site"
FT	Modified-site	14 /note= "Post-translational modification acetylation site"
FT	Modified-site	18 /note= "Post-translational modification acetylation site"
FT	Modified-site	23 /note= "Post-translational modification acetylation site"
FT		
XX		WO200404168-A2.
XX		
PD		27-MAY-2004.
XX		
PF		12-NOV-2003; 2003WO-US036059.
XX		
PR		12-NOV-2002; 2002US-042557AP.
PR		05-AUG-2003; 2003US-00634740.
XX		
PA	(MASI )	MASACHUSETTS INST TECHNOLOGY.
XX		
PI	Ting AY;	
DR		WPI; 2004-420310/39.
XX		
PT	New fusion protein reporter having a core with a histone-modification-	
PT	specific binding domain conjugated to a histone polypeptide, useful for	
PT	diagnosing or treating cancer, viral infections, neurological and	
PT	molecular disorders.	
XX		
PS	Claim 14; SEQ ID NO 1; 96pp; English.	
CC		
CC	The invention relates to a novel fusion protein reporter comprising a	
CC	core having a histone-modification-specific binding domain conjugated to	
CC	a histone polypeptide, wherein the core is flanked by donor and acceptor	
CC	fluorescent moieties. The molecules of the invention demonstrate	
CC	cycostatic, neuroprotective, muscular and virucide activities and may be	
CC	useful for the diagnosis and/or treatment of histone modification-	
CC	associated disorders, such as cancer, neurological disorders, muscular	
CC	disorders, developmental disorders, cell development disorders and	
CC	disorders related to exposure to toxins, toxic chemicals or viruses. The	
CC	current sequence is that of the human histone H3 N-terminal peptide	
CC	ID 1) of the invention.	
XX		
SQ	Sequence 40 AA;	
	Query Match	100.0%; Score 146; DB 8; Length 40;
	Best Local Similarity	100.0%; Pred. No. 3.8e-13;
	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ARTKOTARKSTGCAKPKKATTKARSAKAP 30	
DB	1 ARTKOTARKSTGCAKPKKOLATTKARSAKAP 30	
RESULT 5		
ID	AAU70897	standard; peptide; 55 AA.
XX		
AC	AAU70897;	
XX		
DT	14-FEB-2002	(first entry)
XX		
DE	Histone 2A-derived gene delivery peptide #17.	
XX		

KM Histone 2A; gene therapy; gene delivery; gene therapy; antisense therapy;  
KM nuclear localisation.  
OS Synthetic.  
XX W0200181370-A2.  
XX PN 01-NOV-2001.  
XX PD 24-APR-2001; 2001WO-EP004621.  
XX PF 24-APR-2000; 2000US-0199153P.  
XX PR 24-APR-2000; 2000US-0199153P.  
XX PA (NOVS ) NOVARTIS AG.  
XX PA (NOVS ) NOVARTIS-ERRINDUNGEN VERM GES MBH.  
XX PA (SCRI ) SCRIPPS RES INST.  
XX PI Balicki D, Beutler E;  
XX DR WPI, 2002-055343/07.  
XX PT Histone H2A-derived peptides useful in gene delivery and gene therapy.  
XX PS Example; Fig 1; 37pp; English.  
XX CC The invention relates to an isolated gene delivery facilitating peptide  
XX CC (I) comprising at least 7 amino acids (preferably 17 amino acids) derived  
XX CC from the N-terminal region of Histone H2A, and which exhibits  
XX CC transfection activity and nuclear localisation activity. (I) is useful  
XX CC for delivering a nucleic acid to cells. The gene delivery enhancing  
XX CC peptide, derived from Histone H2A is complexed with a nucleic acid for  
XX CC efficient and stable delivery of the nucleic acid into a cell, ultimately  
XX CC to the nucleus. The peptide mediated gene delivery is based on the  
XX CC principle that un-neutralised positive charges on the histone are bound  
XX CC electro-statically both by the negatively charged phosphate backbone of  
XX CC DNA and that nuclear targeting signals in the histones improve  
XX CC trafficking of the DNA into the nucleus for transfection. This mode of  
XX CC delivery overcomes the limitations of current gene delivery approaches  
XX CC including viral and non-viral means, has minimum toxicity, with cellular  
XX CC access, intracellular trafficking and nuclear retention of plasmids. The  
XX CC entire H2A sequence is not essential for mediating efficient delivery of  
XX CC the nucleic acids into cells as opposed to the prior art use of the full  
XX CC sequence. In addition, substitutions to the sequences have also been  
XX CC found to mediate efficient delivery, providing an improved delivery  
XX CC system on the original H2A protein. AAU70877-AAU70923 represent histone  
XX CC 2A-derived gene delivery peptides used in the method of the invention  
XX CC  
SQ Sequence 55 AA;  
Query Match 100.0%; Score 146; DB 5; Length 55;  
Best local similarity 100.0%; Pred. No. 5,3e-13;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ARTKQTARKSTGGKAPRKQATTKARKSAP 30  
Db 1 ARTKQTARKSTGGKAPRKQATTKARKSAP 30  
RESULT 6  
AA607049  
ID AA607049 standard; protein; 65 AA.  
AC AA607049;  
XX  
XX  
DT 17-OCT-2000 (first entry)  
XX  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 4051.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS

XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
XX PR 05-MAR-1999; 99US-0123180P.  
XX PR 09-MAR-1999; 99US-0123548P.  
XX PR 23-MAR-1999; 99US-0125788P.  
XX PR 23-MAR-1999; 99US-0126264P.  
XX PR 23-MAR-1999; 99US-0126785P.  
XX PR 01-APR-1999; 99US-0127462P.  
XX PR 06-APR-1999; 99US-0128234P.  
XX PR 08-APR-1999; 99US-0128714P.  
XX PR 16-APR-1999; 99US-0129845P.  
XX PR 19-APR-1999; 99US-0130077P.  
XX PR 21-APR-1999; 99US-0130449P.  
XX PR 23-APR-1999; 99US-0130510P.  
XX PR 23-APR-1999; 99US-0131449P.  
XX PR 28-APR-1999; 99US-0132048P.  
XX PR 30-APR-1999; 99US-0132407P.  
XX PR 30-APR-1999; 99US-0132407P.  
XX PR 04-MAY-1999; 99US-0132484P.  
XX PR 05-MAY-1999; 99US-0132485P.  
XX PR 06-MAY-1999; 99US-0132487P.  
XX PR 07-MAY-1999; 99US-0132863P.  
XX PR 11-MAY-1999; 99US-0134256P.  
XX PR 14-MAY-1999; 99US-0134218P.  
XX PR 14-MAY-1999; 99US-0134219P.  
XX PR 14-MAY-1999; 99US-0134221P.  
XX PR 14-MAY-1999; 99US-0134370P.  
XX PR 18-MAY-1999; 99US-0134768P.  
XX PR 19-MAY-1999; 99US-0134941P.  
XX PR 20-MAY-1999; 99US-0135124P.  
XX PR 21-MAY-1999; 99US-0135353P.  
XX PR 24-MAY-1999; 99US-0135629P.  
XX PR 25-MAY-1999; 99US-0136021P.  
XX PR 27-MAY-1999; 99US-0136392P.  
XX PR 28-MAY-1999; 99US-0136782P.  
XX PR 01-JUN-1999; 99US-0137222P.  
XX PR 03-JUN-1999; 99US-0137528P.  
XX PR 04-JUN-1999; 99US-0137502P.  
XX PR 07-JUN-1999; 99US-0137724P.  
XX PR 08-JUN-1999; 99US-0138094P.  
XX PR 10-JUN-1999; 99US-0138540P.  
XX PR 10-JUN-1999; 99US-0138847P.  
XX PR 14-JUN-1999; 99US-0139119P.  
XX PR 16-JUN-1999; 99US-0139452P.  
XX PR 16-JUN-1999; 99US-0139453P.  
XX PR 17-JUN-1999; 99US-0139492P.  
XX PR 18-JUN-1999; 99US-0139454P.  
XX PR 18-JUN-1999; 99US-0139455P.  
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XX PR 18-JUN-1999; 99US-0139457P.  
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Db 33 ARTKQTKARKSTGKAPRKQATTKARKKAP 62

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XX 25-MAR-2003 (reviled)  
DT 19-OCT-1994 (first entry)  
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XX  
XX Human cDNA; library; enzyme; protein.  
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XX  
OS Homo sapiens.  
XX  
PN WO9403599-A1.  
XX  
PD 17-FEB-1994.  
XX  
PF 04-AUG-1993; 93WO-JP001095.  
XX  
PR 04-AUG-1992; 92JP-00208077.

PR 13-NOV-1992; 92JP-00327619.  
PR 26-FEB-1993; 93JP-00061431.  
XX (SAGA ) SAGAMI CHEM RES CENTRE.  
XX Kato S, Oh S, Sekine S, Kim N, Kato T, Iwahori A;  
XX WPI; 1994-065688/08.  
DR N-PSDB; AAG57414.  
XX  
XX cDNA of human origin and proteins coded by it - which may be expressed by  
PT in vivo or in vitro translation using sense RNA or antisense DNA  
PT corresponding to the cDNA.  
XX  
XX Claim 1; Page 29; 167pp; Japanese.  
XX  
XX mRNA expressed in human fibrosarcoma cell line HT-1080 was isolated and  
CC used to construct a cDNA library using vector pX1. Clone HP00014  
CC encoding histone H3.3-like protein was isolated. (Updated on 25-MAR-2003  
CC to correct PN field.)  
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DB 2 ARTKOTARKSTGKAPRKQATKARKSAP 31  
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XX  
DT 18-OCT-2000 (first entry)  
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KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
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XX Arabidopsis thaliana.  
OS  
XX EPI033405-A2.  
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XX  
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DE Zea mays protein fragment SEQ ID NO: 25689.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;  
termination sequence; corn.  
XX  
OS Zea mays subsp. mays.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
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PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 146; DB 3; Length 90;  
Best Local Similarity 100.0%; Pred. No. 8.8e-13;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
Dd 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31

RESULT 10  
ABP42906  
ID ABP42906 standard; protein; 93 AA.  
XX  
AC ABP42906;  
DT 22-AUG-2002 (first entry)  
XX  
DE Human ovarian antigen HPDQX13, SEQ ID NO:4038.  
XX  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KM ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
KM inflammatory condition; immune disorder; blood disorder;  
KM cardiovascular disorder; respiratory disorder; neurological disorder;  
KM gastrointestinal disorder; urinary system disorder; drug screening;  
KM gene therapy; chromosome mapping; forensic analysis;  
KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KM antiinflammatory; gynaecological; reproductive.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
PF 07-JUN-2001; 2001WO-US018569.  
XX  
PR 07-JUN-2000; 2000US-0209467P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
DR WPI: 2002-147878/19.  
DR N-PSDB; ABO55983.  
XX  
XX  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
PT cancer), immune disorders, cardiovascular disorders and neurological  
PT diseases.  
XX  
PS Claim 11; SEQ ID NO 4038; 2922pp; English.  
XX  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 93 AA;  
XX

Query Match 100.0%; Score 146; DB 5; Length 93;  
Best Local Similarity 100.0%; Pred. No. 9.1e-13;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
Dd 4 ARTKQTARKSTGGKAPRKQLATKARKSAP 33

RESULT 11  
AAG13239  
ID AAG13239 standard; protein; 95 AA.  
XX  
AC AAG13239;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 12660.  
DE  
XX  
KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
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PR 04-MAY-1999; 99US-0132484P.  
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PR 06-MAY-1999; 99US-0132486P.



PR 21-OCT-1999; 99US-0160815P.  
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PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161931P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 146; DB 3; Length 95;  
Best Local Similarity 100.0%; Pred. No. 9.3e-13;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30  
Db 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

RESULT 12  
ID AAG01289 standard; protein, 108 AA.  
AC AAG01289;

XX 06-OCT-2000 (first entry)  
XX Human secreted protein, SEQ ID NO: 5370.

DE Human secreted protein, SEQ ID NO: 5370.  
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (G8ST ) GENSET.

XX Dunas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC01295.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 5370; 71bp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNA or polyA<sup>+</sup> RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 146; DB 3; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1.1e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARTKOTARKSTGKAPRKQLATKARKSAP 30  
Db 2 ARTKOTARKSTGKAPRKQLATKARKSAP 31

RESULT 13  
ID AAG54610 standard; protein, 108 AA.  
AC AAG54610;

XX 18-OCT-2000 (first entry)  
XX Zea mays protein fragment SEQ ID NO: 69649.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126254P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

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XX 28-APR-1999; 99US-0130891P.

XX 30-APR-1999; 99US-0131449P.

XX 04-MAY-1999; 99US-0132407P.

XX 04-MAY-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.

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XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134256P.

XX 14-MAY-1999; 99US-0134218P.

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XX 24-MAY-1999; 99US-0135629P.

XX 25-MAY-1999; 99US-0136021P.

XX 27-MAY-1999; 99US-0136392P.

XX 28-MAY-1999; 99US-0136782P.

XX 01-JUN-1999; 99US-0137222P.

XX 03-JUN-1999; 99US-0137528P.

XX 04-JUN-1999; 99US-0137502P.

XX 07-JUN-1999; 99US-0137724P.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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(without alignments)  
73.791 Million cell updates/sec

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- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	55	16	US-10-258-637-20
2	146	100.0	71	17	US-10-425-115-209506
3	146	100.0	83	17	US-10-425-115-238920
4	146	100.0	85	15	US-10-424-599-28206
5	146	100.0	89	17	US-10-425-115-250033
6	146	100.0	90	17	US-10-425-115-218722
7	146	100.0	90	17	US-10-425-115-337375
8	146	100.0	93	15	US-10-264-049-4038
9	146	100.0	94	17	US-10-425-115-336777
10	146	100.0	109	17	US-10-425-115-223514
11	146	100.0	109	17	US-10-425-115-250042
12	146	100.0	117	15	US-10-424-599-254928
13	146	100.0	118	17	US-10-425-115-368708

14	146	100.0	128	17	US-10-425-115-333644	Sequence 333644,
15	146	100.0	130	17	US-10-425-115-250032	Sequence 250032,
16	146	100.0	134	17	US-10-425-115-250036	Sequence 250036,
17	146	100.0	136	9	US-09-864-761-47600	Sequence 47600, A
18	146	100.0	136	15	US-10-424-599-143601	Sequence 143601,
19	146	100.0	136	15	US-10-424-599-146317	Sequence 146317,
20	146	100.0	136	15	US-10-424-599-150528	Sequence 150528,
21	146	100.0	136	15	US-10-424-599-152778	Sequence 152778,
22	146	100.0	136	15	US-10-424-599-175415	Sequence 175415,
23	146	100.0	136	15	US-10-424-599-175418	Sequence 175418,
24	146	100.0	136	15	US-10-424-599-185675	Sequence 185675,
25	146	100.0	136	15	US-10-424-599-201020	Sequence 201020,
26	146	100.0	136	15	US-10-424-599-220706	Sequence 220706,
27	146	100.0	136	15	US-10-424-599-240645	Sequence 240645,
28	146	100.0	136	15	US-10-424-599-248782	Sequence 248782,
29	146	100.0	136	15	US-10-424-599-252539	Sequence 252539,
30	146	100.0	136	15	US-10-424-599-254930	Sequence 254930,
31	146	100.0	136	15	US-10-424-599-254931	Sequence 254931,
32	146	100.0	136	15	US-10-424-599-256890	Sequence 256890,
33	146	100.0	136	15	US-10-205-331-12	Sequence 12, Appl
34	146	100.0	136	16	US-10-701-490-10	Sequence 10, Appl
35	146	100.0	136	16	US-10-437-963-130283	Sequence 130283,
36	146	100.0	136	16	US-10-437-963-134798	Sequence 134798,
37	146	100.0	136	16	US-10-437-963-152369	Sequence 152369,
38	146	100.0	136	16	US-10-437-963-152371	Sequence 152371,
39	146	100.0	136	16	US-10-437-963-152374	Sequence 152374,
40	146	100.0	136	16	US-10-767-701-46471	Sequence 46471, A
41	146	100.0	136	16	US-10-767-701-46533	Sequence 46533, A
42	146	100.0	136	16	US-10-767-701-46719	Sequence 46719, A
43	146	100.0	136	16	US-10-767-701-46721	Sequence 46721, A
44	146	100.0	136	16	US-10-767-701-46854	Sequence 46854, A
45	146	100.0	136	16	US-10-767-701-46905	Sequence 46905, A

#### ALIGNMENTS

RESULT 1  
US-10-258-637-20  
Sequence 20, Application US/10258637  
Publication No. US20040102606A1  
GENERAL INFORMATION:  
APPLICANT: Beutler, Ernest  
TITLE OF INVENTION: Histone H2A-derived peptides useful in gene delivery  
FILE REFERENCE: T8RI 743.1  
CURRENT APPLICATION NUMBER: US/10/258, 637  
CURRENT FILING DATE: 2002-10-24  
PRIOR APPLICATION NUMBER: PCT/EP01/04621  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: US 60/199,153  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 55  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: synthetic histone-derived peptide  
US-10-258-637-20

Query Match 100.0%; Score 146; DB 16; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1,1e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKQTKARKSTGKAPRKQLATKARKSAP 30  
Db 1 ARTKQTKARKSTGKAPRKQLATKARKSAP 30

RESULT 2  
US-10-425-115-209506

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/ Sequence 209506, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 209506
/ LENGTH: 71
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(71)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_122663C.1.pep
US-10-425-115-209506
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Query Match          100.0%; Score 146; DB 17; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 5 ARTKQTARKSTGGKAPPRKQLATKARKSAP 34
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RESULT 3
US-10-425-115-238920
/ Sequence 238920, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 238920
/ LENGTH: 83
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_149484C.1.pep
US-10-425-115-238920
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```
Query Match          100.0%; Score 146; DB 17; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 2 ARTKQTARKSTGGKAPPRKQLATKARKSAP 31
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```
RESULT 4
US-10-424-599-282206
/ Sequence 282206, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
```

```
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 265684
/ SEQ ID NO 282206
/ LENGTH: 85
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(85)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_96855C.1.pep
US-10-424-599-282206
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Query Match          100.0%; Score 146; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 38 ARTKQTARKSTGGKAPPRKQLATKARKSAP 67
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```
RESULT 5
US-10-425-115-250033
/ Sequence 250033, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 250033
/ LENGTH: 89
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_159614C.1.pep
US-10-425-115-250033
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```
Query Match          100.0%; Score 146; DB 17; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ARTKQTARKSTGGKAPPRKQLATKARKSAP 30
Db 2 ARTKQTARKSTGGKAPPRKQLATKARKSAP 31
```

```
RESULT 6
US-10-425-115-218722
/ Sequence 218722, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
```

```

; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 218722
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_131066C.1.pep
US-10-425-115-218722

Query Match          100.0%; Score 146; DB 17; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
    |||||
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31

RESULT 7
US-10-425-115-337375
; Sequence 337375, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 337375
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70856C.1.pep
US-10-425-115-337375

Query Match          100.0%; Score 146; DB 17; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
    |||||
Db 35 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 64

RESULT 8
US-10-264-049-4038
; Sequence 4038, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Blise et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264.049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4038
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: MISC_FEATURE
; LOCATION: (45)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (50)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4038

Query Match          100.0%; Score 146; DB 15; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
    |||||
Db 4 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 33

RESULT 9
US-10-425-115-336777
; Sequence 336777, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336777
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70288C.1.pep
US-10-425-115-336777

Query Match          100.0%; Score 146; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
    |||||
Db 7 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 36

RESULT 10
US-10-425-115-223514
; Sequence 223514, Application US/10425115
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```
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 223514
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_135434C.1.pep
US-10-425-115-223514
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Query Match          100.0%; Score 146; DB 17; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
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```
RESULT 11
US-10-425-115-250042
/ Sequence 250042, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 250042
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(109)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: MRT4577_159622C.1.pep
US-10-425-115-250042
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Query Match          100.0%; Score 146; DB 17; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
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```
RESULT 12
US-10-424-599-254928
/ Sequence 254928, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
```

```
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 254928
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)-(117)
/ OTHER INFORMATION: unsure at all Xaa locations
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_72222C.1.pep
US-10-424-599-254928
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Query Match          100.0%; Score 146; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
```

```
RESULT 13
US-10-425-115-368708
/ Sequence 368708, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 368708
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_99435C.1.pep
US-10-425-115-368708
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Query Match          100.0%; Score 146; DB 17; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 30
Db 2 ARTKOTARKSTGGKAPRKQLATKAAKRSAP 31
```

```
RESULT 14
US-10-425-115-333644
/ Sequence 333644, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 333644  
 ; LENGTH: 128

; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(128)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_67396C.1.pep  
 US-10-425-115-333644

Query Match 100.0%; Score 146; DB 17; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKAARKSAP 30  
 DB 2 ARTKOTARKSTGGKAPRKQLATKAARKSAP 31

# RESULT 15

US-10-425-115-250032  
 ; Sequence 250032, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 250032  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(130)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_159613C.1.pep  
 US-10-425-115-250032

Query Match 100.0%; Score 146; DB 17; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 2,7e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKAARKSAP 30  
 DB 2 ARTKOTARKSTGGKAPRKQLATKAARKSAP 31

Search completed: December 23, 2004, 11:39:02  
 Job time : 150 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 11:13:09, Search time 39 Seconds

(Without alignments)  
74.013 Million cell updates/sec

Title: US-10-634-740-18

Perfect score: 146  
Sequence: 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	146	100.0	35	2 A39525	histone H3 - mouse
2	146	100.0	39	2 I48113	histone H3.2 - Chi
3	146	100.0	48	2 A61286	histone H3 - sea u
4	146	100.0	48	2 C61286	histone H3 - cycad
5	146	100.0	48	2 B61286	histone H3 - sandp
6	146	100.0	60	2 S51664	histone H3.3 - tom
7	146	100.0	62	2 B38309	histone H3.2 - alf
8	146	100.0	76	2 A38309	histone H3.1 - alf
9	146	100.0	121	2 A02630	histone H3 - bovin
10	146	100.0	135	1 HSB03	histone H3 - Alen
11	146	100.0	135	1 HSEA3	histone H3 - Alen
12	146	100.0	135	1 HSF13	histone H3 - small
13	146	100.0	135	1 HSPW3	histone H3 - garde
14	146	100.0	135	1 HSRK3	histone H3 - scip
15	146	100.0	135	1 HSRK3	histone H3, gonada
16	146	100.0	135	1 HSR3M	histone H3, embryo
17	146	100.0	135	1 HSR3P	histone H3, embryo
18	146	100.0	135	1 HSR31	histone H3.1 - Alf
19	146	100.0	135	2 JQ1963	H3.3 like histone
20	146	100.0	135	2 S00373	histone H3 - wheat
21	146	100.0	136	1 HSKW3	histone H3 - Caeno
22	146	100.0	136	1 HSKW3	histone H3 - chick
23	146	100.0	136	1 HSHU3	histone H3.3 [vali
24	146	100.0	136	1 HSHU3	histone H3.3 - hum
25	146	100.0	136	2 A56880	histone H3 - midge
26	146	100.0	136	2 S09655	histone H3 - fruit
27	146	100.0	136	2 S10097	histone H3 - fruit
28	146	100.0	136	2 A56618	histone H3 - spoon
29	146	100.0	136	2 A56654	histone H3 - Tigr1

30	146	100.0	136	2 S06743	histone H3 - mouse
31	146	100.0	136	2 I49397	histone H3.2 prote
32	146	100.0	136	2 I49398	histone H3.1 prote
33	146	100.0	136	2 I57019	H3 histone - rat
34	146	100.0	136	2 S61218	histone H3.3 - fru
35	146	100.0	136	2 S61220	histone H3.3 - fru
36	146	100.0	136	2 S01198	histone H3 - starf
37	146	100.0	136	2 S20678	histone H3 - starf
38	146	100.0	136	2 I50245	histone H3.3B - ch
39	146	100.0	136	2 S01196	histone H3 - starf
40	146	100.0	136	2 S01197	histone H3 - starf
41	146	100.0	136	2 S20669	histone H3.3 - starf
42	146	100.0	136	2 S50140	histone H3 - sea
43	146	100.0	136	2 JN0687	histone H3 - sea
44	146	100.0	136	2 S10168	histone H3.3A - ra
45	146	100.0	136	2 S56707	histone H3 homolog

#### ALIGNMENTS

##### RESULT 1

A39525 histone H3 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 12-Apr-1995  
C/Accession: A39525  
R/Mahadevan, L.C.; Willis, A.C.; Barratt, M.J.  
Cell 65, 775-783, 1991  
A>Title: Rapid histone H3 phosphorylation in response to growth factors, phorbol esters  
A/Reference number: A39525; PMID:91249384; PMID:2040014  
A/Accession: A39525  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-35 <MAH>  
C/Superfamily: histone H3  
C/Keywords: chromosomal protein; nucleosome core

Query Match 100.0%; Score 146; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.5e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
DB 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30

##### RESULT 2

I48113 histone H3.2 - Chinese hamster (fragment)  
C/Species: Cricetus griseus (Chinese hamster)  
C/Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 21-Jul-2000  
C/Accession: I48113  
R/Artibeveky, A.; Wooden, S.; Sharma, A.; Resendez, E.  
Nature 328, 823-827, 1987  
A>Title: Cell-cycle regulatory sequences in a hamster histone promoter and their intera  
A/Reference number: I48113; PMID:87315341; PMID:3627229  
A/Accession: I48113  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-39 <RES>  
A/Cross-references: GB:M28265; NID:9341874; PIND:AAA42371.1; PID:9554580  
C/Genetics:  
A/Gene: H3.2  
C/Superfamily: histone H3

Query Match 100.0%; Score 146; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.6e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKQTARKSTGGKAPRKQLATKARKSAP 30  
DB 2 ARTKQTARKSTGGKAPRKQLATKARKSAP 31



A/Residues: 1-76 <MAT>  
A/Cross-references: UNIPROT:P02300  
A/Superfamily: histone H3  
C/Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 100.0%; Score 146; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30  
Db 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30

RESULT 9

A02630  
histone H3 - fruit fly (*Drosophila melanogaster*) (fragments)  
C/Species: *Drosophila melanogaster*  
C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C/Accession: A02630  
R/Goldberg, M.L.  
Ph.D. thesis, Stanford Univ., 1979  
A/Reference number: A02630  
A/Molecule type: DNA  
A/Residues: 1-121 <GOL>  
A/Cross-references: UNIPROT:P02299  
A/Note: the author translated the codon CCC for residue 31 as Ala  
C/Genetics:  
A/Gene: *FLYBase:H33*  
A/Cross-references: *FLYBase:FBgn0001199*  
C/Superfamily: histone H3  
C/Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 100.0%; Score 146; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 4.5e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30  
Db 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30

RESULT 10

HSB03  
histone H3 - bovine  
C/Species: *Bos primigenius taurus* (cattle)  
C/Date: 08-Oct-1981 #sequence\_revision 08-Oct-1981 #text\_change 09-Jul-2004  
C/Accession: A02624; PLO130; R49978; S68319  
R/Delange, R.J.; Hooper, J.A.; Smith, E.L.  
J. Biol. Chem. 248, 3261-3274, 1973  
A/Title: Histone III. III. Sequence studies on the cyanogen bromide peptides; complete a  
A/Reference number: A92132; PMID:7316574; PMID:4735580  
A/Accession: A02624  
A/Molecule type: protein  
A/Residues: 1-135 <DEL>  
A/Cross-references: UNIPROT:P16106  
A/Note: Cys-96 and Cys-110 can form an intrachain disulfide bond or interchain disulfide  
A/Note: Lys-23 is acetylated in 43% of the molecules and Lys-14, in an unknown percent  
R/Pardoll, W.M.; Nowlin, D.M.; Calaycay, J.; Shively, J.E.  
J. Neurochem. 53, 1014-1018, 1989  
A/Title: Predominant low-molecular-weight proteins in isolated brain capillaries are his  
A/Reference number: PLO130; PMID:85361419; PMID:2769252  
A/Accession: PLO130  
A/Molecule type: protein  
A/Residues: 1-16 <PAR>  
A/Experimental source: brain  
R/Makim, B.T.; Aswad, G.D.  
J. Biol. Chem. 269, 2722-2727, 1994  
A/Title: Ca(2+)-calmodulin-dependent phosphorylation of arginine in histone 3 by a nucle  
A/Reference number: A49978; PMID:9413040; PMID:8300603  
A/Accession: A49978  
A/Molecule type: protein

A/Residues: 1-24;121-135 <MAK>  
R/Delange, R.J.; Smith, E.L.  
J. Biol. Chem. 248, 3248-3254, 1973  
A/Title: Histone III. I. Isolation and sequences of the tryptic peptides from the maley  
A/Reference number: A92130; PMID:7316572; PMID:4735579  
A/Contents: annotation; tryptic peptides  
R/Hooper, J.A.; Smith, E.L.  
J. Biol. Chem. 248, 3255-3260, 1973  
A/Title: Histone III. II. Isolation and sequences of chymotryptic peptides from calf th  
A/Reference number: A92131; PMID:7316573; PMID:4700459  
A/Contents: annotation; chymotryptic peptides  
R/Marzluft Jr., W.F.; Sanders, L.A.; Miller, D.M.; McCarty, K.S.  
J. Biol. Chem. 247, 2026-2033, 1972  
A/Title: Two chemically and metabolically distinct forms of calf thymus histone F3.  
A/Reference number: A92102; PMID:72154496; PMID:5016641  
A/Contents: annotation; thymus, variant  
A/Note: 20% of the histone H3 fraction consists of a minor form that differs from that  
R/Patthy, L.; Smith, E.L.  
J. Biol. Chem. 250, 1919-1920, 1975  
A/Title: Histone III. IV. Two forms of calf thymus histone III.  
A/Reference number: A92174; PMID:75095680; PMID:1167550  
A/Contents: annotation; variant  
A/Note: analyses of two chymotryptic peptides, both corresponding to positions 91-99, i  
R/Coupez, M.; Belatche, D.  
Arch. Biochem. Biophys. 325, 29-38, 1996  
A/Title: Successive elution by ion-exchange chromatography of H3-H4 histone complexes d  
A/Reference number: S68319; PMID:96140594; PMID:8554340  
A/Accession: S68319  
A/Molecule type: protein  
A/Residues: 1-29 <COU>  
C/Superfamily: histone H3  
C/Keywords: acetyllysine; chromosomal protein; DNA binding; methylated amino acid; nucl  
F/2,128,129,131/Binding site: phosphate (Arg) (covalent) #status experimental  
F/9,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine  
F/14,23/Binding site: acetyl (Lys) (covalent) (partial) #status experimental  
F/96,110/Disulfide bonds: interchain (in polymeric form) #status experimental  
F/96-110/Disulfide bonds: (in monomeric form) #status experimental

Query Match 100.0%; Score 146; DB 1; Length 135;  
Best Local Similarity 100.0%; Pred. No. 5e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30  
Db 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30

RESULT 11

HSEAH3  
histone H3 - Altensein's bread tree  
C/Species: *Enephalartos altenseinii* (Altensein's bread tree)  
C/Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
C/Accession: A23604  
R/Brandt, W.F.; von Holt, C.  
FEBS Lett. 194, 278-281, 1986  
A/Title: The primary structure of histone H3 from cycad pollen.  
A/Reference number: A23604  
A/Accession: A23604  
A/Molecule type: protein  
A/Residues: 1-135 <BRA>  
A/Cross-references: UNIPROT:P08903  
A/Experimental source: pollen  
A/Note: 53-Lys, 96-Ser, 107-Ser, and 124-Val were also found  
C/Superfamily: histone H3  
C/Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome core  
F/4/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status expe  
F/9,27/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) #status experimenta

Query Match 100.0%; Score 146; DB 1; Length 135;  
Best Local Similarity 100.0%; Pred. No. 5e-12;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARTKOTARKSTGGAPRKQATKAARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

## RESULT 12

HSR13

histone H3 - smallmouth buffalo fish

C/Species: Ictiobus bubalus (smallmouth buffalo fish)

C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

C/Accession: A02627

R/Author: J.A.; Smith, E.L.; Sommer, K.R.; Chalkley, R.

J. Biol. Chem. 248, 3275-3279, 1973

A/Title: Histone III. IV. Amino acid sequence of histone III of the testes of the carp.

A/Reference number: A02627; PMID:7316575; PMID:4700460

A/Accession: A02627

A/Molecule type: protein

A/Residues: 1-135 &lt;HOO&gt;

A/Cross-references: UNIPROT:P16105

A/Note: Lys-9 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth

A/Note: Lys-27 is epsilon-N-monomethyllysine, epsilon-N-dimethyllysine, epsilon-N-trimeth

C/Superfamily: histone H3

C/Keywords: chromosomal protein; DNA binding; methylated amino acid; nucleosome core

F/9,27/Modified site: N6-methyllysine, N6,N6-dimethyllysine or N6,N6,N6-trimethyllysine

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

## RESULT 13

HSPM3

histone H3 - garden pea (tentative sequence)

C/Species: Pisum sativum (garden pea)

C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004

C/Accession: A02631

R/Author: L.; Smith, E.L.; Johnson, J.

J. Biol. Chem. 248, 6834-6840, 1973

A/Title: Histone III. V. The amino acid sequence of pea embryo histone III.

A/Reference number: A02631; PMID:74011270; PMID:4795661

A/Accession: A02631

A/Molecule type: protein

A/Residues: 1-135 &lt;PMT&gt;

A/Cross-references: UNIPROT:P02300

A/Experimental source: embryo

A/Note: Lys-9 and Lys-27 are mainly epsilon-N-monomethyllysine. In a small fraction of

C/Superfamily: histone H3

C/Keywords: chromosomal protein; DNA binding; nucleosome core

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

## RESULT 14

HSRK3

histone H3 - striped catshark

C/Species: Poroderma africanum (striped catshark)

C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

C/Accession: A02626

R/Author: W.F.; Strickland, W.N.; von Holt, C.

FEBS Lett. 40, 349-352, 1974

A/Title: The primary structure of histone F3 from shark erythrocytes.

A/Reference number: A02626; PMID:74309063; PMID:4855011

A/Accession: A02626

A/Molecule type: protein

A/Residues: 1-135 &lt;BRA&gt;

A/Cross-references: UNIPROT:P16105

A/Note: Lys-9 (70%), Lys-27 (50%), and Lys-36 (20%) are methylated, mainly with the dim

C/Comment: The amount and position of acetylation was not precisely determined. Electroy

C/Superfamily: histone H3

C/Keywords: acetyllysine; chromosomal protein; DNA binding; methylated amino acid; nuclc

F/9,27,36/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #statu

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

## RESULT 15

HSR13

histone H3, gonadal - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)

C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004

C/Accession: B92959; B93779; B23220

R/Author: W.; States, J.C.; Mezquita, J.; Dixon, G.H.

J. Mol. Evol. 20, 236-250, 1984

A/Title: Organization and nucleotide sequence of rainbow trout histone H2A and H3 genes

A/Reference number: A92959; PMID:85083109; PMID:6439879

A/Accession: B92959

A/Molecule type: DNA

A/Residues: 1-135 &lt;CON&gt;

A/Cross-references: UNIPROT:P16105; GB:X01064; NID:964324; PIDN:CMA25529.1; PID:964326

A/Note: Initiator Met not shown

R/Candido, E.P.M.; Dixon, G.H.

Proc. Natl. Acad. Sci. U.S.A. 69, 2015-2019, 1972

A/Title: Amino-terminal sequences and sites of in vitro acetylation of trout-testis histc

A/Reference number: A93779; PMID:72259090; PMID:4506069

A/Accession: B93779

A/Molecule type: protein

A/Residues: 1-25 &lt;CAN&gt;

C/Superfamily: histone H3

C/Keywords: acetyllysine; chromosomal protein; DNA binding; nucleosome core; testis

F/9,18/Binding site: acetyl (Lys) (covalent) (partial) #status experimental

F/14,23/Binding site: acetyl (Lys) (covalent) #status experimental

Query Match 100.0%; Score 146; DB 1; Length 135;

Best Local Similarity 100.0%; Pred. No. 5e-12; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Db 1 ARTKOTARKSTGGKAPRKQLATKARKSAP 30

Search completed: December 23, 2004, 11:22:49

Job time : 40 secs